Amendment Under 37 C.F.R. § 1.111 Attorney Docket No.: Q63915

U.S. Appln. 09/820,843

AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the

application:

LISTING OF CLAIMS:

1.-19. (Canceled).

20. (New) A method for identifying a candidate protein useful as an anti-infective,

comprising:

(a) calculating computationally protein sequence-based attributes from all protein

sequences of a pathogenic organism, wherein said protein sequence-based attributes are selected

from a group consisting of percentage of charged amino acids, percentage hydrophobicity,

distance of protein sequence from a fixed reference frame, measure of dipeptide complexity, and

measure of hydrophobicity from a fixed reference frame;

(b) clustering computationally said all protein sequences based on said protein sequence-

based attributes using Principle Component Analysis;

(c) identifying computationally outlier proteins, wherein said outlier proteins appear

outside a main cluster;

(d) comparing said outlier proteins to known proteins to identify a unique outlier protein;

and

(e) validating said unique outlier protein as an anti-infective.

2

Amendment Under 37 C.F.R. § 1.111 Attorney Docket No.: Q63915 U.S. Appln. 09/820,843

- 21. (New) The method of claim 20, wherein said pathogenic organism is selected from the group consisting of B.burgdorfei, C.jejuni, C.pneumoniae, C.trachomatis, H.influenzae, H.pylori, L.major, M.genitalium, M.pneumoniae, M.tuberculosis, N.menigitis, P.aeruginosa, P.falciparum, R.prowazekii, T.pallidum, and V.cholerae.
- 22. (New) The method of claim 20, wherein said protein sequence-based attributes are selected from the group consisting of fixed protein attributes and variable protein attributes.
- 23. (New) The method of claim 22, wherein a variable protein attribute is a distance of protein sequence from a variable reference frame.
- 24. (New) The method of claim 20, wherein said clustering is done by Principle Component Analysis using correlation coefficient between said protein sequence-based attributes.
- 25. (New) The method of claim 20, wherein said clustering is based upon analysis of protein sequence-based attributes and not based upon sequence pattern linked to biochemical functions.
- 26. (New) The method of claim 20, wherein said unique outlier protein is non-homologous to known anti-infective proteins from a pathogen selected from the group consisting of B.burgdorfei, C.jejuni, C.pneumoniae, C.trachomatis, H.influenzae, H.pylori, L.major, M.genitalium, M.pneumoniae, M.tuberculosis, N.menigitis, P.aeruginosa, P.falciparum, R.prowazekii, T.pallidum, and V.cholerae.

Amendment Under 37 C.F.R. § 1.111 U.S. Appln. 09/820,843

Attorney Docket No.: Q63915

- 27. (New) The method of claim 20, wherein said unique outlier protein has an amino acid sequence selected from the group consisting of SEQ ID Nos: 1-31.
- 28. (New) The method of claim 20, wherein said unique outlier protein has an amino acid sequence selected from the group consisting of SEQ ID Nos: 32-118.
- 29. (New) The method of claim 20, wherein steps are performed by a computer system comprising:
- (1) a central processing unit (CPU), wherein said CPU executes DISTANCE program and clusters protein sequences based on protein sequence-based attributes using Principle Component Analysis, thereby producing results;
 - (2) a memory device accessed by said CPU, wherein said memory device stores said results;
 - (3) a display on which said CPU displays said results in response to user inputs; and
 - (4) a user interface device.
- 30. (New) The method of claim 20, wherein said unique outlier protein may be used for a diagnostic purpose.
- 31. (New) The method of claim 20, wherein said unique outlier protein may be used as a vaccine candidate.

Amendment Under 37 C.F.R. § 1.111 U.S. Appln. 09/820,843

Attorney Docket No.: Q63915

32. **(New)** The method of claim 20, wherein said unique outlier protein may be used for a therapeutic purpose.

33. (New) The method as of claim 20, wherein said unique outlier protein can elicit an immune response.